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Two new species of the genus *Scincella* Mittleman, 1950 (Squamata, Scincidae) from southwestern China

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Abstract

The genus *Scincella* Mittleman, 1950 of the family Scincidae is a species-rich group currently comprising 51 recognized species. In this study, we describe two new species of *Scincella* from southwestern Sichuan, China: *Scincella jinchuanensis* **sp. nov.** and *Scincella maerkangensis* **sp. nov.** *Scincella jinchuanensis* **sp. nov.**, collected from Jinchuan County, Sichuan Province, is phylogenetically most closely related to the recently described *S. heishuiensis*. It can be distinguished morphologically by possessing a high number of subdigital lamellae on the fourth toe (17–18), and genetically by an uncorrected pairwise distance of 3.82% in 16S rRNA and 13.7% in COI. *Scincella maerkangensis* **sp. nov.**, collected from Maerkang City, Sichuan Province, is phenotypically similar to *S. wangyuezhaoi*. It differs from the latter in having fewer midbody scale rows and shows a genetic divergence of 6.38% (16S rRNA) and 14.8% (COI). Together with *S. wangyuezhaoi* and *S. heishuiensis*, the two new species form a distinct lineage that is clearly separate from other congeners included in the study, with interspecific divergence in 16S rRNA sequences exceeding 3%. The discovery of these two new species raises the number of *Scincella* species recorded in China to 19, further underscoring the significant reptilian diversity in the Hengduan Mountain region.

Key Words

Comparative morphology, Hengduan Mountains, mitochondrial DNA, phylogenetic relationships

Introduction

Despite the growing number of newly discovered species, some biodiversity hotspots – such as the Hengduan Mountains and the Himalayas – remain poorly studied. The Hengduan Mountains (HDM), located on the eastern Qinghai–Xizang Plateau (QXP), exhibit dramatic elevational gradients that produce distinct vertical ecological zones and harbour exceptionally high biodiversity (Liu et al. 2018; Wang et al. 2019; Jia et al. 2023, 2024, 2025; Guo et al. 2019, 2020, 2025; Liu et al. 2026).

The genus *Scincella* Mittleman, 1950, which is one of the genera within the family Scincidae, currently comprises 51 species and exhibits a broad distribution across East Asia, Southeast Asia, and North America (Uetz et al. 2025). This genus is characterized by several distinct morphological traits: a transparent disk on the lower eyelid, smooth cycloid scales, relatively short limbs, an elongated body, and a small body size. It commonly inhabits forest edges near streams, arid-hot valleys in the Hengduan Mountains, and areas around exposed rocks in grasslands.

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In China, the HDM represents the primary distribution area for *Scincella* species. Zhao et al. (1999) and Wang et al. (2020) documented 14 species of *Scincella* in China. Based on molecular phylogeny, Che et al. (2020) reclassified three species (*S. ladacensis*, *S. himalayanus*, and *S. sikimmensis*) into the genus *Asymblepharus*, which was later synonymized with *Ablepharus* by Mirza et al. (2022). Presently, there are 16 species of *Scincella* recorded in China, with 10 species documented in Sichuan Province.

During recent fieldwork in the HDM, we collected a batch of *Scincella* specimens from western Sichuan, China. Based on morphological examination and molecular genetic analyses, we identified these specimens as two distinct taxa and hereby describe them as new species below.

Materials and methods

Specimens collection

Ten specimens of *Scincella* were collected from Jinchuan County (six) and Maerkang City (four), Sichuan Province, China (Fig. 1). After the liver was extracted, the specimens were fixed in a 10% formaldehyde solution for three days and then transferred to 80% ethanol for long-term preservation. The liver samples were preserved in 85% ethanol at –80 °C. All specimens and samples are deposited at Yibin University (**YBU**).

Morphology examination

The 10 unidentified specimens were morphologically examined and recorded following Zhao et al. (1999) and Nguyen et al. (2019). Body dimensions were taken with a digital caliper to the nearest 0.1 mm. Symmetrical mensural head characters were taken on the right side of the head only unless this was damaged, in which case they were taken on the left. Meristic characters were recorded on both sides, and the average was used in the analysis. All data were collected by the senior author to avoid inter-observer bias.

The characters measured and recorded and their abbreviations are as follows: snout–vent length (SVL, distance from tip of snout to posterior edge of vent); tail length (TAL, distance from posterior margin of vent to tip of tail); axilla–groin distance (AGD, distance between posterior edge of forelimb insertion and anterior edge of hindlimb insertion); forelimb length (FLL, measured from

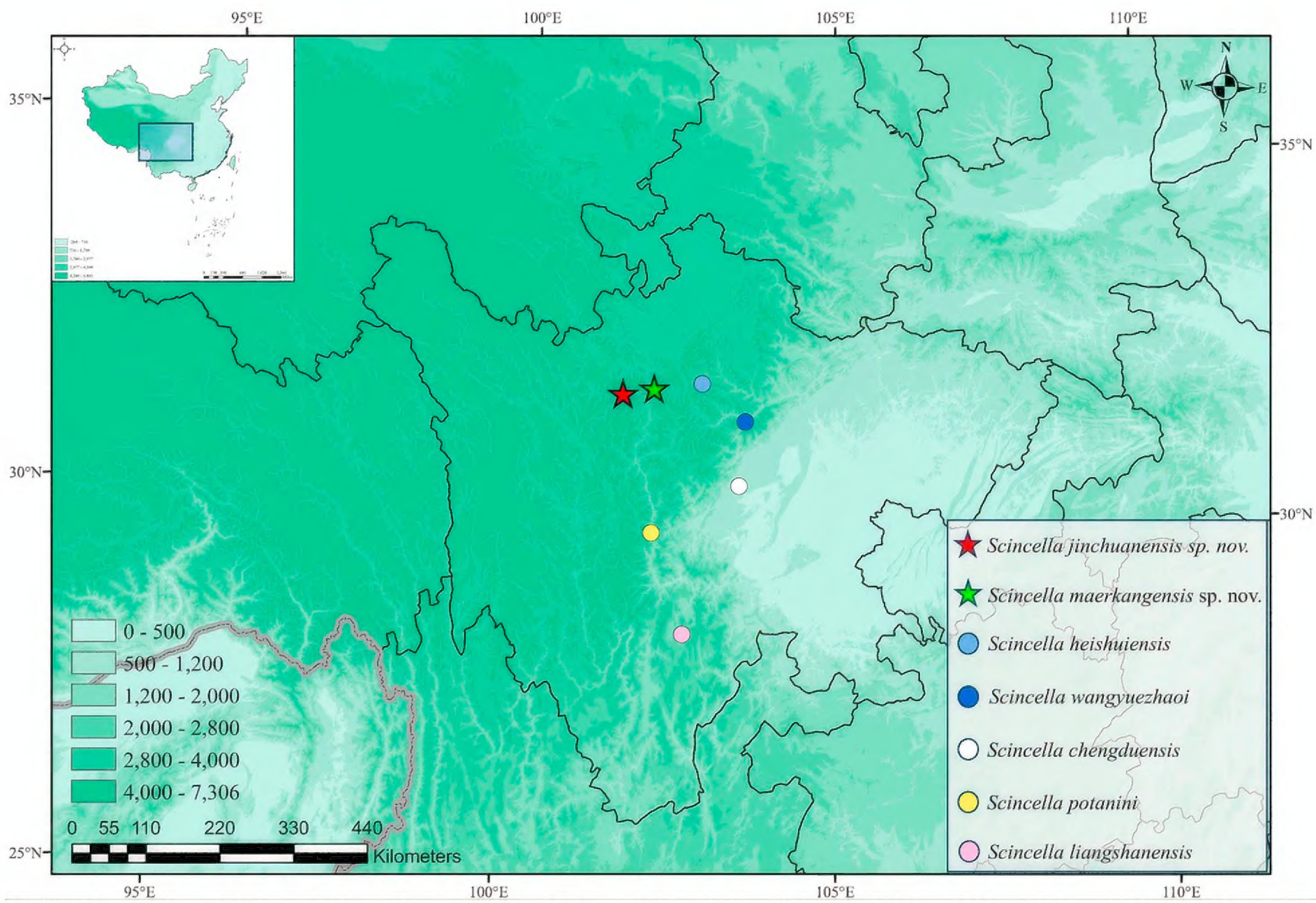

Figure 1. A map showing the type localities of the genus *Scincella* species in the Hengduan Mountain region of southwestern China. *Scincella jinchuanensis* sp. nov. is located in Jinchuan County, Aba Prefecture, Sichuan Province; *Scincella maerkangensis* sp. nov. in Maerkang City, Aba Prefecture, Sichuan Province; *S. heishuiensis* in Heishui County, Aba Prefecture, Sichuan Province; *S. wangyuezhaoi* in Wenchuan County, Aba Prefecture, Sichuan Province; *S. chengduensis* in Chengdu City, Sichuan Province; *S. potanini* in Kangding City, Garzê Prefecture, Sichuan Province; and *S. liangshanensis* in Yuexi County, Liangshan Yi Autonomous Prefecture, Sichuan Province. Elevation data were sourced from the Geospatial Data Cloud (2024).

forelimb insertion to tip of finger IV or longest digit); hindlimb length (HLL, measured from hindlimb insertion to tip of toe IV or longest digit); toe IV length (T4L, measured from the most basal part to the tip of toe IV); finger IV length (F4L, measured from the most basal part to the tip of finger IV); midbody scale-row count (MBSR, number of longitudinal scale rows measured around the widest point of midbody); dorsal scale rows between dorsolateral stripes (DBR, number of dorsal scale rows at midbody between dark dorsolateral stripes, following Inger); enlarged, differentiated nuchal count (NU, X pairs or absence); paravertebral scale-row count (PVSR, number of scale rows counted between parietals and the posterior margin of the hindlimbs); ventral scale-row count (VSR, number of scale rows counted between gulars and precloacal scales); superciliary count (SC, left/right); supralabial count (SL, left/right); infralabial count (IfL, left/right); superciliary count (SC, left/right); supraocular count (SO, left/right); enlarged temporal count (TEM, left/right); number of enlarged, undivided lamellae beneath finger IV (F4S, left/right); number of enlarged, undivided lamellae beneath toe IV (T4S, left/right); frontoparietal in contact with each other (FP); prefrontal in contact with each other (PF); chin-shields: paired large scales behind mental or postmentals; gulars: many minor scales in the center of the ventral head (number of scale rows counted between the first scale behind the chin-shields and the middle of the forelimb); appearance of dorso-lateral stripes (ADLS).

For morphological comparison, the characters of the other species were from published data (Gray 1838; Zhao and Huang 1982; Inger et al. 1990; Darevsky and Orlov 1997; Zhao et al. 1999; Zhao 2003; Nguyen et al. 2010; Neang et al. 2018; Jia et al. 2023, 2024; Xu et al. 2025).

Molecular analyses

Total DNA was extracted from the liver tissue of 10 samples using the M5 HiPer Universal DNA Mini Kit (Mei5 Biotechnology Co., Ltd). Four mitochondrial DNA fragments were amplified: 12S ribosomal RNA (12S) using primers L1091-F and H1478-R (5′–3′: AAACTGGGATTAGATACCCCACTAT/GAGGGTGACGGGCGGTGTGT) (Kocher et al. 1989), 16S ribosomal RNA (16S) using primers 16SL-F and 16SL-R (5′–3′: TGTTTACCAAAAACATAGCCTTTAGC/TAGATAGAAACCGACCTGGATT) (Linkem et al. 2011), cytochrome *c* oxidase subunit I (COI) using primers Chmf4 and Chmr4 (5′–3′: TYTCWACWAAYCAYAAAGAYATCGG/ACYTCRGGRTGRCCRAARAATCA) (Che et al. 2012). PCR cycling parameters followed the original protocols from these studies. PCR products were purified using commercial kits prior to sequencing. Bidirectional sequencing was performed by Sangon Biotech (Shanghai, China). Sequence editing was conducted in Lasergene v15.1 (DNASTAR Inc.), followed by ClustalW alignment and quality verification in MEGA v11.0 (Tamura et al. 2021). Additional sequences for 23 *Scincella* species and one outgroup, *Sphenomorphus cryptotis*, were retrieved from GenBank and included in the subsequent analyses (Darevsky et al. 2004; Pyron et al. 2013; Koizumi et al. 2022) (Table 1).

Prior to phylogenetic analyses, the optimal substitution model for each gene partition was selected using PartitionFinder 2.1.1 (Lanfear et al. 2017) under the Akaike Information Criterion. Phylogenetic trees were constructed using Maximum likelihood (ML) and Bayesian inference (BI) methods. BI analyses were conducted in MrBayes 3.1.2 (Ronquist et al. 2012) using three heated chains and one cold chain, with three independent runs of 10 million generations each (sampling every 2000 generations). The initial 25% of samples were discarded as burn-in, with the average standard deviation of split frequencies falling below 0.005 and the potential scale reduction factor (PSRF) approaching 1.000. ML analysis was performed in RAxML v7.2.6 (Stamatakis 2014) using the GTRGAMMA model under the same partitioning scheme as in the BI analysis. Node support was assessed with 1000 nonparametric bootstrap replicates (Hillis and Bull 1993). The validity of the Bayesian results was further confirmed as the effective sample sizes (ESS) of all parameters exceeded 200.

To assess the genetic divergence between taxa, uncorrected pairwise genetic distances (*p*-distances) for the 16S rRNA gene sequences were calculated using MEGA 11 (Tamura et al. 2021).

Results

Morphology examination

The newly collected specimens share features diagnostic of the genus *Scincella*, such as well-developed eyelids, the absence of supranasal scales, and the presence of one pair of preanal scales. However, these specimens could be separated into two distinct groups, each diagnosable by a combination of unique morphological characters, such as dorsal scale rows between dark dorsolateral stripes (DBR) at midbody and subdigital lamellae on the fourth toe.

Molecular phylogeny

The final aligned dataset comprised 520 bp from 16S rRNA, 353 bp from 12S rRNA, and 619 bp from COI. The best-fit nucleotide substitution model for the concatenated dataset was GTR+I+G. All novel sequences generated in this study have been deposited in GenBank (Table 1).

Both BI and ML analyses yielded generally consistent phylogenetic topologies, with minor discrepancies in some shallow nodes (Fig. 2). All recognized *Scincella* species, including all newly collected specimens, formed a strongly supported monophyletic group (1.00 BS and 95% PP). *Scincella jinchuanensis* sp. nov. and *S. heishuiensis* form a strongly supported sister lineage (BS = 100, PP = 1.00), whereas *Scincella maerkangensis* sp. nov.,

Table 1. Detailed information for all samples used in this study.

Species	Locality	Voucher ID	16S	12S	COI
Scincella maerkangensis sp. nov.	China:Sichuan, Maerkang City	YBU 250139	PX570716	PX570727	PX578840
Scincella maerkangensis sp. nov.	China:Sichuan, Maerkang City	YBU 250140	PX570717	PX570728	PX578841
Scincella maerkangensis sp. nov.	China:Sichuan, Maerkang City	YBU 250141	–	PX570729	PX578842
Scincella maerkangensis sp. nov.	China:Sichuan, Maerkang City	YBU 250143	PX570718	PX570730	PX578843
Scincella jinchuanensis sp. nov.	China: Sichuan, Jinchuan	YBU 22314	PX570712	PX570723	PX529354
Scincella jinchuanensis sp. nov.	China: Sichuan, Jinchuan	YBU 22315	PX570713	PX570724	PX529355
Scincella jinchuanensis sp. nov.	China: Sichuan, Jinchuan	YBU 22316	PX570714	PX570725	PX529356
Scincella jinchuanensis sp. nov.	China: Sichuan, Jinchuan	YBU 22317	PX570715	PX570726	PX529357
Scincella jinchuanensis sp. nov.	China: Sichuan, Jinchuan	YBU 22292	PX570710	PX570721	PX529352
Scincella jinchuanensis sp. nov.	China: Sichuan, Jinchuan	YBU 250959	PX570711	PX570722	PX529353
Scincella heishuiensis	China: Sichuan, Heishui	YBU 22269	PX285308	PX285312	PX285297
Scincella heishuiensis	China: Sichuan, Heishui	YBU 22275	PX285309	PX285313	PX285298
Scincella chengduensis	China: Sichuan, Dayi	CIB 107637	PQ466921	PQ466924	PQ467109
Scincella chengduensis	China: Sichuan, Chongzhou	CIB 118786	PQ466920	PQ466923	PQ467108
Scincella liangshanensis	China: Sichuan, Yuexi	XM-YXS80	PP826313	PP826316	PP824805
Scincella liangshanensis	China: Sichuan, Meigu	CIB 119513	PP826315	PP826317	PP824806
Scincella qianica	Baiyun District, Guizhou, China	QHU R2025001	PV527321	PV527316	PV527759
Scincella qianica	Baiyun District, Guizhou, China	QHU R2025002	PV527322	PV527317	PV527760
Scincella alia	Tay Con Linh Mt., Ha Giang, Vietnam	VRTC NAP14081	–	–	PV085567
Scincella alia	Tay Con Linh Mt., Ha Giang, Vietnam	ZMMU Re-18153	PV088913	PV088911	PV085569
Scincella badenensis	Vietnam: Tay Ninh, Ba Den Mountain	ITBCZ 5966	–	–	MK990602
Scincella gemmingeri	–	–	AY308294	–	–
Scincella badenensis	Vietnam: Tay Ninh, Ba Den Mountain	ITBCZ 5993	–	–	MK990603
Scincella baraensis	Vietnam: Binh Phuoc, Ba Ra Mountain	ITBCZ 6534	–	–	MT742256
Scincella baraensis	Vietnam: Binh Phuoc, Ba Ra Mountain	ITBCZ 6536	–	–	MT742258
Scincella boettgeri	Japan: Southern-Ryukyu Islands, Yaeyama Group	KUZ R68001	–	–	LC630768
Scincella boettgeri	Japan: Southern-Ryukyu Islands, Yaeyama Group	KUZ R68008	–	–	LC630770
Scincella cherriei	Mexico: Chiapas, Montes Azules Biosphere Reserve	RCMX235	MW265932	–	–
Scincella doriae	Vietnam: Lam Dong, Bidoup-Nui Ba N. P.	ZMMU R-13268-01062	–	–	MH119617
Scincella doriae	Vietnam: Lam Dong, Bidoup-Nui Ba N. P.	ZMMU R-13268-00412	–	–	MH119616
Scincella dunan	Japan: Southern Ryukyus, Yonagunijima Is.	KUZ R65170	–	–	LC630778
Scincella dunan	Japan: Southern Ryukyus, Yonagunijima Is.	KUZ R67027	–	–	LC630779
Scincella formosensis	China: Taiwan	KUZ R37516	–	–	LC630790
Scincella formosensis	China: Taiwan	KUZ R37515	–	–	LC630789
Scincella lateralis	–	KU 289460	JF498077	JF497948	–
Scincella lateralis	USA: Texas	DCC 2842	HM852503	HM852476	–
Scincella melanosticta	Vietnam: Gia Lai, Kon Chu Rang N.R.	ZMMU NAP-06376	–	–	MH119622
Scincella melanosticta	Vietnam: Gia Lai, Kon Chu Rang N.R.	ZMMU NAP-05519	–	–	MH119621
Scincella fansipanensis	Vietnam: Lao Cai Province, Fansipan	IEBR R.5185	–	–	LC846671
Scincella fansipanensis	Vietnam: Lao Cai Province, Fansipan	IEBR R.5187	–	–	LC846672
Scincella modesta	China: Zhejiang, Ningpo	WYF 11520		PP819197	PP819215
Scincella modesta	China: Zhejiang, Ningpo	CIB 121415	PP819195	PP819198	PP819217
Scincella monticola	China: Yunnan, Shangri-La	DL-YNJC2020824	OP955962	OP955952	–
Scincella nigrofasciata	Vietnam: Ba Ria-Vung Tau, Dinh Mountain	ITBCZ 6344	–	–	MK990605
Scincella nigrofasciata	Cambodia: Mondulkiri, Keo Seima W.S.	CBC 02546	–	–	MH119614
Scincella potanini	China: Sichuan, Kangding	DL-KD202109071	OP935937	OP942203	OP942210
Scincella potanini	China: Sichuan, Kangding	DL-KD202109072	OP935987	OP942208	OP942209
Scincella vandenburghi	Japan: Tsushima Is.	KUZ R66394	–	–	LC507695
Scincella huanrenensis	Korea: Gangwon-do, Pyeongchang-gun	G390SH	NC030779	NC030779	NC030779
Scincella huanrenensis	Korea: Gangwon-do, Pyeongchang-gun	–	KU507306	KU507306	KU507306
Scincella tsinlingensis	China: Gannan Tibetan Autonomous Prefecture, Gansu Province	GP8387	PX570708	PX570719	PX532266
Scincella tsinlingensis	China: Gannan Tibetan Autonomous Prefecture, Gansu Province	GP8388	PX570709	PX570720	PX532315
Scincella wangyuezhaoi	China: Sichuan, Wenchuan	CIB 87246	OP941172	OP942191	OQ402205
Scincella wangyuezhaoi	China: Sichuan, Lixian	CIB 119518	OP941173	OP942193	–
Scincella wangyuezhaoi	China: Sichuan, Lixian	CIB 119510	OP941174	OP942192	OQ402206
Sphenomorphus cryptotis	China: Guangxi, Shangsi	CIB 119027	OP942190	OP942206	OP942215

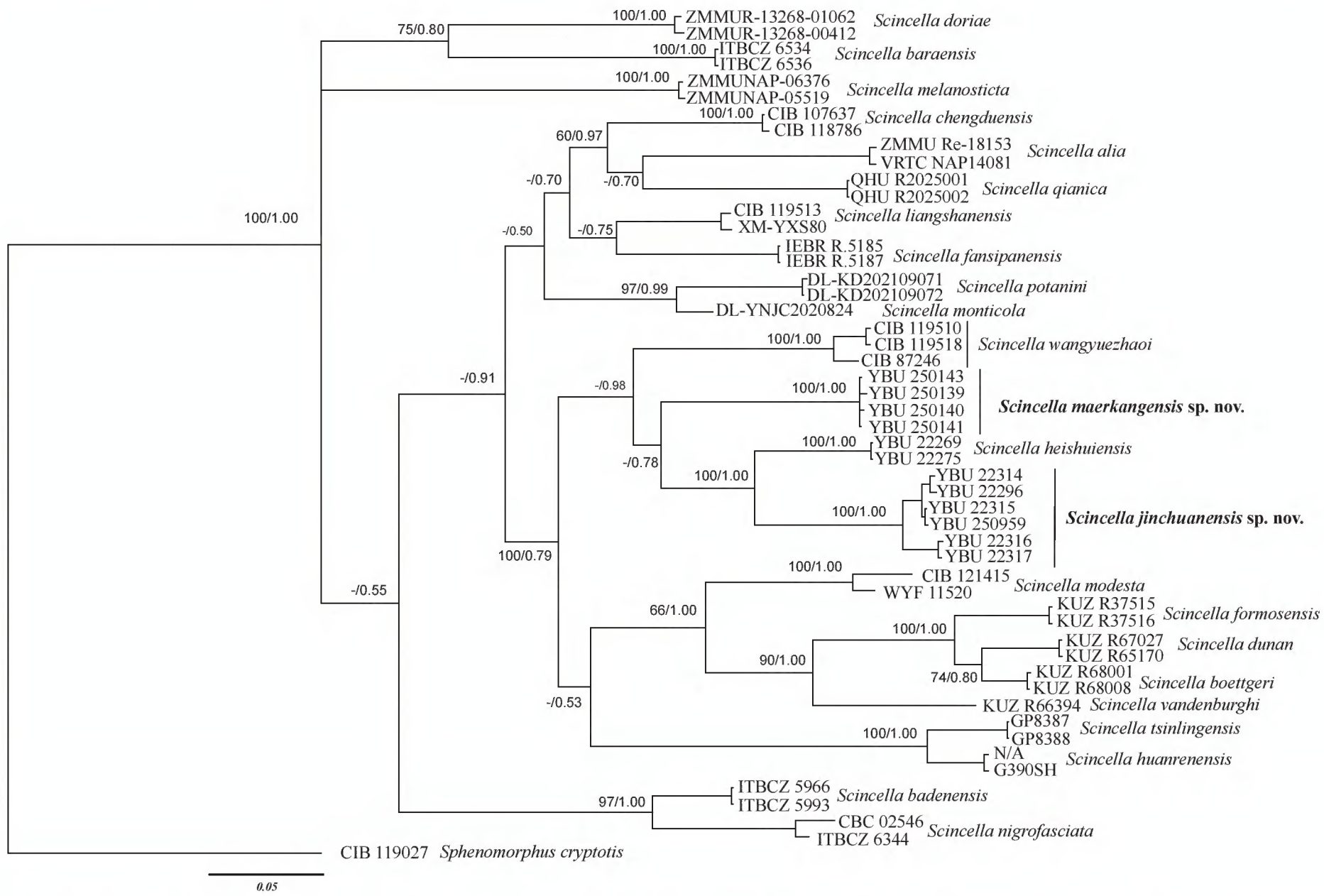

Figure 2. Phylogenetic tree reconstructed based on three mitochondrial fragments. Ultrafast bootstrap supports (BS) from ML analyses and Bayesian posterior probabilities (PP) from BI analyses are shown above branches (BS/PP). Values lower than 50 are displayed as "–".

Scincella jinchuanensis sp. nov., *S. heishuiensis*, and *S. wangyuezhaoi* together comprise a single clade.

Based on 16S rRNA sequence, interspecific genetic distances among *Scincella* species (two unidentified lineages as two taxa) ranged from 2.19% (*S. tsinlingensis* vs. *S. huanrenensis*) to 10.18% (*S. huanrenensis* vs. *S. gemmingeri*). The two unidentified lineages exhibit genetic divergence of 5.12% (Jinchuan) and 6.38% (Maerkang) with *S. wangyuezhaoi*, and the genetic distance to *S. heishuiensis* is 3.82% (Jinchuan) and 6.17% (Maerkang) (Table 2).

Based on COI sequences, the interspecific genetic distances among *Scincella* species (with two unidentified lineages treated as separate taxa) ranged from 12.5% (*S. fansipanensis* vs. *S. liangshanensis*) to 23.1% (*S. melanosticta* vs. *S. vandenburghi*). The genetic divergence between the two unidentified lineages and *S. wangyuezhaoi* was 17.1% (Jinchuan) and 14.8% (Maerkang), respec-

Table 2. Uncorrected *p*-distances (%) between species of *Scincella* based on 16s RNA sequence.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1. *Scincella jinchuanensis* sp. nov.															
2. *Scincella maerkangensis* sp. nov.	6.74														
3. *S. heishuiensis*	3.82	6.17													
4. *S. wangyuezhaoi*	5.12	6.38	5.45												
5. *S. liangshanensis*	6.33	7.08	6.00	6.21											
6. *S. chengduensis*	6.66	6.85	5.68	5.81	2.94										
7. *S. assata*	9.09	8.94	9.93	9.40	8.48	7.71									
8. *S. potanini*	8.21	8.48	8.32	8.44	6.66	5.46	8.61								
9. *S. tsinlingensis*	8.44	10.11	8.55	8.46	8.21	8.10	7.96	8.77							
10. *S. monticola*	6.88	8.46	7.21	7.99	5.12	4.79	8.37	3.28	7.44						
11. *S. lateralis*	7.95	8.58	7.08	8.54	8.06	7.28	8.74	8.52	9.49	6.95					
12. *S. gemmingeri*	8.43	9.48	8.17	9.18	7.82	7.93	7.93	8.83	9.73	8.81	8.09				
13. *S. huanrenensis*	8.90	10.13	9.01	8.85	8.22	7.46	8.43	8.13	2.19	7.02	10.40	10.18			
14. *S. qianica*	7.18	7.33	6.78	6.77	5.13	3.93	9.27	6.35	8.11	5.68	8.30	9.05	7.91		
15. *S. alia*	5.79	8.69	5.90	6.97	3.59	3.70	8.59	6.77	8.32	4.79	7.17	8.59	8.11	4.37	

Table 3. Uncorrected *p*-distances (%) between species of *Scincella* based on COI sequences.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1. *Scincella jinchuanensis* sp. nov.																				
2. *S. maerkangensis* sp. nov.	17.3																			
3. *S. heishuiensis*	13.7	14.6																		
4. *S. wangyuezhaoi*	17.1	14.8	15.2																	
5. *S. chengduensis*	17.0	17.1	15.6	18.1																
6. *S. liangshanensis*	19.2	15.9	15.3	16.4	16.1															
7. *S. alia*	17.9	17.0	16.7	18.4	15.3	15.6														
8. *S. qianica*	18.8	18.4	17.3	15.7	16.3	14.8	15.9													
9. *S. nigrofasciata*	20.0	18.8	18.3	17.8	18.7	17.5	17.6	19.8												
10. *S. potanini*	15.8	15.2	15.6	16.4	17.0	13.7	17.4	17.2	17.1											
11. *S. modesta*	17.9	16.8	16.0	17.0	18.4	16.3	18.4	19.2	19.2	17.3										
12. *S. tsinlingensis*	18.1	18.2	17.0	18.8	17.8	16.5	19.0	18.8	19.5	18.8	19.7									
13. *S. vandenburghi*	19.5	19.1	16.8	17.0	16.3	16.8	17.9	19.9	18.9	16.9	15.6	19.9								
14. *S. boettgeri*	18.8	18.1	19.0	20.4	18.3	16.8	17.9	19.7	19.1	15.9	15.8	18.3	14.1							
15. *S. dunan*	18.9	18.2	18.0	19.8	18.4	19.0	19.0	20.3	19.0	18.6	16.3	18.3	15.1	7.6						
16. *S. formosensis*	18.9	18.9	18.2	20.2	18.3	18.7	18.4	19.5	20.0	18.7	17.1	16.9	14.4	8.8	9.6					
17. *S. fansipanensis*	17.9	15.0	16.4	16.4	16.7	12.5	15.7	16.8	16.2	14.5	16.4	18.4	17.7	16.8	18.7	18.8				
18. *S. doriae*	17.6	19.5	17.6	20.2	19.6	17.0	16.1	19.4	17.5	16.8	16.9	20.9	17.0	18.4	19.1	19.4	18.3			
19. *S. melanosticta*	19.7	21.2	21.3	21.2	20.0	18.6	19.0	20.5	21.0	18.9	20.7	21.3	23.1	20.5	21.9	21.2	20.1	19.1		
20. *S. badenensis*	18.6	17.6	18.6	18.2	19.2	17.7	18.8	17.9	10.7	18.9	20.0	19.3	21.1	19.5	19.2	20.2	16.6	19.1	19.8	
21. *S. baraensis*	19.6	21.5	19.2	20.8	21.8	17.6	20.8	20.1	18.7	18.3	19.9	21.6	21.2	20.8	22.4	20.6	18.7	16.8	19.0	18.9

tively, while their genetic distances from *S. heishuiensis* were 13.7% (Jinchuan) and 14.6% (Maerkang) (Table 3).

Based on integration of morphological comparison and molecular phylogeny, we conclude that the two unidentified lineages represent two distinct, undescribed species. They are formally described below.

Scincella jinchuanensis sp. nov.

https://zoobank.org/A08DEC7B-E312-4515-A380-93110669B6A9

Figs 3–6

Type material. ***Holotype.*** • YBU 22317, male, collected from Jinchuan County, Aba Tibetan and Qiang Autonomous Prefecture, Sichuan Province, China (31.8213°N, 101.6319°E, 2906 m a.s.l.), in May 2022.

Paratypes. • (n = 3). YBU 22316 and YBU 250959, adult males; YBU 22292 adult female. The same locality, date, and collectors as the holotype.

Diagnoses. *Scincella jinchuanensis* sp. nov. exhibits the following characteristics which can distinguish from its congeners. (1) 6 dorsal scale rows between dorsolateral stripes; (2) 28 Midbody scale rows; (3) Lamellae beneath 4th finger 10–11, beneath 4th toe 17–18; (4) Supraoculars 4–5; (5) Superciliarys 0–6; (6) Supralabials 7–9; (7) Infralabials 6–8; (8) Paravertebral scales 58–86; (9) Ventral scales 56–64; (10) Its scales are finer than those of other species.

Description of the holotype. YBU 22317, an adult male. The body is slender and medium sized, with a snout-vent length (SVL) of 40.01 mm and tail length (TAL) of 73.59 mm (TAL/SVL 1.84). The neck is indistinct from the head. The nasal scale is rhomboidal, contacting both the first supralabial scale and the rostral scale. Nuchal scales five. The axilla-groin distance (AGD) is 25.26 mm in length (AGD/SVL 0.63). The forelimb length (FLL) is 6.04 mm, and the hindlimb length (HLL) is 10.92 mm. Forelimb digit lengths: IV > III > II > V > I; Hindlimb digit lengths: IV > III > II > V > I. Fingers are slender, F4L 2.12 mm, T4L 4.65 mm. Subdigital lamellae single, arranged in an overlapping series: F4S 11/11, T4S 18/17.

The rostral is blunt and rounded. Prefrontals 2, rhomboid-shaped, separated by the frontonasal, with the two scales contacting only at a point. Frontoparietals 2, irregularly pentagonal, in contact with each other. Supraoculars 4/5. Parietal 1, the largest scale on the dorsal head, pentagonal in shape, with a width approximately two-thirds of its length; its lateral margins contact supraoculars and prefrontals. Five asymmetrical nuchals, arranged in a 2/3 pattern, all elongated (approximately three times longer than wide), the first pair largest. The supranasal and postnasals are absent, the ear opening is oval, larger than the palpebral window but smaller than the eye diameter, and the anterior edge of the ear opening lacks flap-like protrusions; the tympanic membrane is recessed. Loreals 2/2. The lower eyelid has a distinct transparent disc (window), and both eyelids are accompanied by minute scales. Superciliaris 4/0, unilaterally absent superciliary scales. The nasal is oval, the nostril positioned at its center. Supralabials 7/7, the first contacts the nasal, 6th largest. Temporals 4(3+1), upper first row larger and contacts the parietal. Infralabials 7/7, slender and elongated, with the first being the smallest. The gulars 25, gular scales relatively small and off-white in color. The mental scale is broad, occupying the anterior edge of the lower jaw; there is one larger postmental. Three pairs of chin shields, the first pair in medial contact, the second and third pairs separated by a small scale.

Body scales smooth, MBSR 28; dorsal scales widened, larger than the lateral and ventral scales 86, dorsal scales

Figure 3. Holotype of *Scincella jinchuanensis* sp. nov. (YBU 22317) in life.

Figure 4. A. Dorsal and **B.** Ventral views of the holotype of *Scincella jinchuanensis* sp. nov. (YBU 22317) in preservative.

between dorso-lateral stripes 6; ventral scales slightly enlarged medially, decreasing toward the flanks, ventral scales 62 rows; there are two larger preanal scales, overlapped by the lateral precloacals, and the left scale overlaps the right; tail base thick. Limbs pentadactyl, toes not in contact with fingers when limbs adpressed; digits slender.

Coloration of the holotype in life. The dorsal head and tail display a distinct bronze coloration, with a bronze patch extending from the nostril to the eye. All dorsal head scales are smooth and bear black spots. The dorsum is bronze and scattered with black spots. Irregular dark dorsal patterns, formed by melanin-rich scales, are present on the anterior body and tail, including prominent ventrolateral stripes. A continuous lateral stripe runs from behind the eye to the tail base. The ventral side features a silver-gray throat and is otherwise uniformly silver-white, devoid of spots.

After preservation in formaldehyde and alcohol, the head and dorsum appear uniformly dark brown. The throat and abdomen are bright gray, the limbs are bronze, and the area near the cloaca on the tail is light gray.

Intraspecific variation. The variation of metrical characteristics of the type series is provided in Table 4. The holotype differs from the paratypes by having five supraoculars on one side, while all others have four. Additionally, the holotype lacks superciliaris on one side, a characteristic not observed in the paratypes.

Etymology. The species is named after its type locality in Jinchuan County, Sichuan Province, China. We suggested the common names "金川滑蜥" in Chinese and "Jinchuan ground skink" in English for this species.

Distribution and ecology. Currently, this species is known only from Jinchuan County, Sichuan, China.

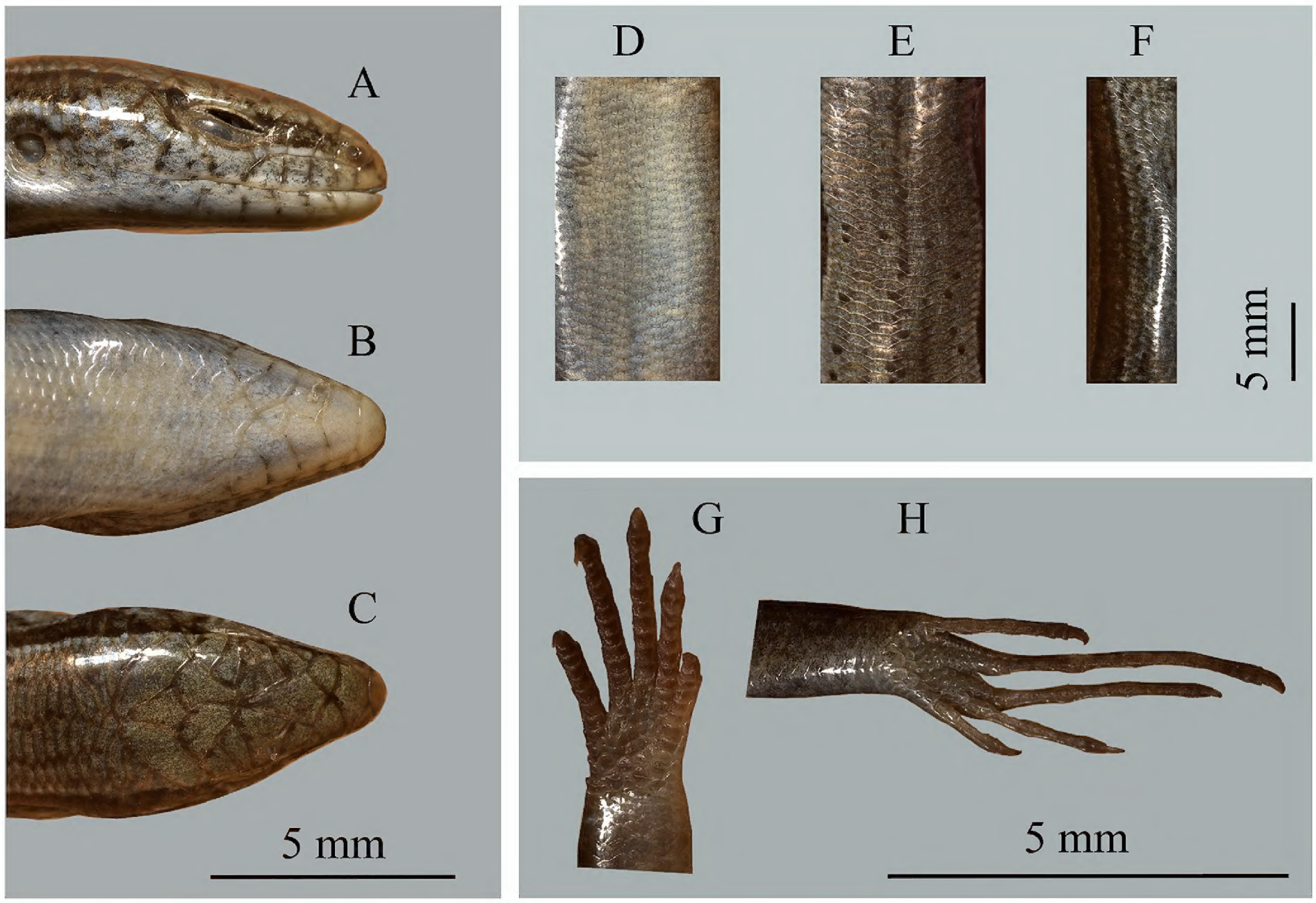

Figure 5. Holotype of *Scincella jinchuanensis* sp. nov. (YBU 22317). **A.** Dorsal; **B.** Ventral, and **C.** Lateral views of the head; **D.** Dorsal; **E.** Ventral, and **F.** Lateral views of the midbody; **G.** Ventral view of hand and **H.** Foot.

The type specimens were collected in late May 2022. They inhabit areas near small shrublands and show a preference for large rocks as shelter. Individuals bask on exposed rock surfaces when these are illuminated by sunlight (Fig. 6). The species occurs sympatrically with *Protobothrops jerdonii*.

Comparisons with congeners. In addition to its large genetic distances, *Scincella jinchuanensis* sp. nov. can be distinguished from all known congeners based on distinct morphological characters. Notably, it differs from *S. heishuiensis*, *S. tsinlingensis*, *S. potanini*, *S. monticola*, *S. qianica*, *S. huanrenensis*, *S. chengduensis*, *S. fansipanensis*, *S. liangshanensis*, and *S. schmidti* by having more dorsal scale rows between dorsolateral stripes 1/2+6+1/2 (vs. 1/2+4+1/2).

The new species can also be distinguished from *S. przewalskii* by having 4–5 supraoculars (vs. 3). It is different from *S. monticola*, *S. potanini*, *S. qianica*, and *S. doriae* by exhibiting 28 midbody scale-row (vs. 23–24 in *S. monticola*, 24–27 in *S. potanini*, 26 in *S. qianica*, 30–32 in *S. doriae*). *Scincella jinchuanensis* sp. nov. can be differentiated from *S. reevesii*, *S. modesta*, *S. doriae*, *S. schmidti*, *S. barbouri*, and *S. formosensis* by having straight dorso-lateral stripes (vs. wavy). The new species is different from *S. heishuiensis*, *S. potanini*, *S. monticola*, *S. schmidti*, *S. alia*, *S. qianica*, *S. chengduensis*, *S. fansipanensis*, and *S. liangshanensis* by having a greater

Figure 6. Type locality habitat of *Scincella jinchuanensis* sp. nov. in Jinchuan County, Sichuan Province, China.

number of enlarged, undivided lamellae beneath toe IV, 17–18 (vs. 13–14 in *S. heishuiensis*; 10–13 in *S. potanini*; 10–12 in *S. monticola*; 11–12 in *S. schmidti*; 11–13 in *S. alia*; 13–14 in *S. qianica*; 10–12 in *S. chengduensis*; 10–12 in *S. fansipanensis*; 10–15 in *S. liangshanensis*), and further from *S. chengduensis* by having more gulars 23–25 (vs. 21–22).

The new species is most similar to *S. wangyuezhaoi*, but it can be distinguished from *S. wangyuezhaoi* by having fewer gulars 23–25 (vs. 25–30), a greater number of enlarged, undivided lamellae beneath toe IV (17–18 vs. 14–15), and fewer scale rows covered by dorsolateral stripes (2 vs. 3) (Table 4).

Table 4. Measurements and scale counts of the type specimens of *Scincella jinchuanensis* sp. nov. Abbreviations are detailed in the section of materials and methods.

Characters	Holotype	Paratypes		
	YBU22317	YBU22316	YBU250959	YBU22292
SVL	40.01	40.19	46.69	49.35
TAL	73.59	59.35	70.28	–
FLL	6.04	6.36	6.34	7.98
HLL	10.92	10.42	8.72	9.63
AGD	25.26	23.25	23.63	26.47
NU	2–3	3–2	3–2	3–3
SL	7–7	7–7	8–7	7–7
IFL	7–7	6–6	7–7	7–6
F4L	2.12	2.13	2.36	2.55
T4L	4.65	4.64	4.65	5.12
SC	4–0	6–2	5–7	4–6
SO	4–5	4–4	4–4	4–4
L	2–2	2–2	2–2	2–2
PN	0	0	0	0
MBSR	28	28	28	28
DBR	1/2+6+1/2	1/2+6+1/2	1/2+6+1/2	1/2+6+1/2
TEM	1+3/1+3	2+2/2+2	1+3/1+3	1+3/1+3
SRB	2	2	2	2
PVSR	86	77	58	70
T4S	18–17	17–17	18–17	17–17
F4S	11–11	11–11	11–13	10–11
GL	25	25	24	23
VSR	62	64	55	62
PF	2	2	2	2
FP	2	2	2	2
ADLS	straight	straight	straight	straight

Scincella maerkangensis sp. nov.

https://zoobank.org/3A95BEAA-24D4-4604-AB7C-BC3C14263375

Figs 7–10

Type material. ***Holotype.*** • YBU 250140, adult female, collected from Maerkang City, Aba Tibetan and Qiang Autonomous Prefecture, Sichuan Province, China (31.8881°N, 101.1116°E, 3197 m a.s.l.), in May 2025.

Paratypes. • (n = 3). YBU 250143, YBU 250141 adult males; YBU 250139, female. The same locality, date, and collectors as the holotype.

Diagnoses. *Scincella maerkangensis* sp. nov. exhibits the following characteristics which can distinguish from its congeners: (1) 4 dorsal scale rows between dorsolateral stripes; (2) Midbody scale 24 rows; (3) Lamellae beneath 4th finger 10–12, beneath 4th toe 14–15; (4) Supraoculars 4–4; (5) Superciliarys 4–7;(6) Supralabials7–9; (7) Infralabials 6–8; (8) Paravertebral scale 58–67 rows; (9) Ventral scale 51–61 rows; (10) A longer tail relative (TAL/SVL 1.40).

Description of the holotype. Adult female, SVL 50.18 mm; the tail is longer, TAL 71.90 mm, TAL/SVL 1.43; the limbs are shorter, HLL 9.72 mm on left, HLL/SVL 0.19, FLL 6.42 mm on left side, FLL/SVL 0.13. AGD 29.27 mm, the body is slender, with the limbs adpressed without contact between them. Forelimb digit lengths: IV > III > II > V > I; hindlimb digit lengths: IV > III > II > V > I.

The snout is wider than it is high, with the dorsal aspect visible and in contact with the first supranasal, nasal, and prenasal scales; it is trapezoidal in shape, with a width approximately twice its height, in contact with rostral, nasals, anterior loreals, prefrontals, and frontal; the supranasal is absent, nasal scales intact, nostrils at bottom; loreals 2–2, the nasal scale is oval, with the nostril located close to the loreal scale, separated from 1st supralabial by single row of scales on each side. prefrontals 2, in contact with each other anteriorly. bordered by frontal, 2nd to 4th supraoculars, frontoparietal, and parietals; frontal slender, longer than wide, diamond-shaped, in contact with the first supraoculars laterally, supraoculars 4–4 with the 2nd largest; tympanic membrane sunken. Supralabials 8/9, the first contacts the nasal, 6th largest; infralabials 8/6, slender and elongated, with the first being the smallest. Five asymmetrical nuchals, arranged in a 2/3 pattern, all elongated (approximately three times longer than wide), the first pair largest; lower eyelid bearing an undivided transparent window, surrounded small palpebral scales; temporals 4(3+1), upper first row larger and contacts the parietal; chin shields in three pairs and the third pair separated by three gulars; the gulars 25, gular scales relatively small.

Body scales smooth, midbody scale-row 24, paravertebral scale-row 60; dorsal scale rows between dorsolateral stripes 1/2+4+1/2. ventral scale-row 56, enlarged preanal scale pairs one, median scales overlapping outer scales, tail base thick, gradually tapering from the middle toward the tip. The subcaudals at the base of the tail are nearly equal in size and arranged alternately along the midline; dorsal surface of the fourth finger and toe mostly covered with two rows of supradigital scales, with the terminal two scales arranged in a single row. Subdigital lamellae single, arranged in an overlapping series: enlarged undivided lamellae beneath toe IV 11/11, enlarged undivided lamellae beneath toe 14/15.

Coloration of the holotype in life. In its wild state, the dorsal surface of the head is copper-colored, scattered with irregular small blackish-brown spots. The upper lateral head is blackish brown, gradually fading to brown below, and speckled with irregular blackish-brown spots. The ventral side of the head is creamy white, with several large blackish-brown spots. The edges of the infralabials, chin shields, and some lateral gular scales are blackish

Figure 7. Paratype of *Scincella maerkangensis* sp. nov. in life.

Figure 8. A. Dorsal and **B.** Ventral views of the holotype of *Scincella maerkangensis* sp. nov. (YBU 250140) in preservative.

brown, forming approximately several discontinuous longitudinal stripes. The dorsal surface of the body is copper-colored, with three longitudinal stripes composed of continuous but irregular black spots of varying sizes. The lateral stripes are more distinct and continuous, extending from the postocular region to the mid-tail section. The mid-dorsal stripe is discontinuous, composed of black pigmentation on individual scales, and extends only to the base of the tail. The flanks are pale gray in ground color, speckled with minute black spots, while the ventrolateral region exhibits a uniformly distributed blackish-gray hue. The spotting gradually sparse out towards the ventral area and disappears near the mid-venter. The venter is silver-gray with non-overlapping, distinctly keeled scales.

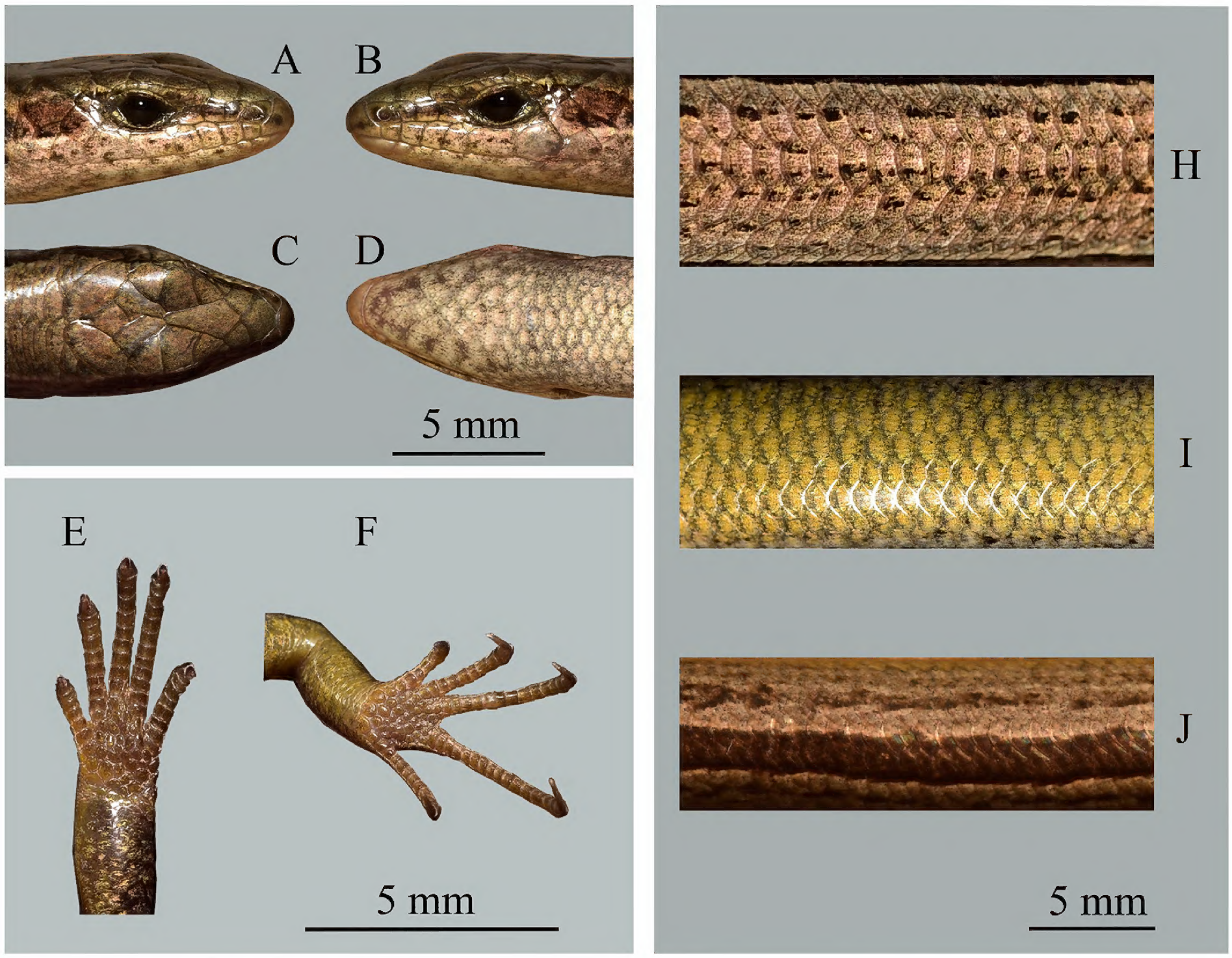

Figure 9. Holotype of *Scincella maerkangensis* sp. nov. (YBU 250140). **A.** Right lateral; **B.** Left lateral; **C.** Dorsal, and **D.** Ventral views of the head; **E.** Ventral view of hand and **F.** Foot; **H.** Dorsal; **I.** Ventral, and **J.** Lateral views of the midbody.

After preservation in formaldehyde and alcohol, the head and dorsum adopt a uniform brown hue with intensified lateral dark stripes. The dorsum and venter retain smooth integument texture, while the tail is lateral and ventral surfaces develop dark brown to black spotting. Throat and belly bright gray, limbs bronze, and caudal region near the cloaca pale gray.

Intraspecific variation. The paratype differs only slightly from the holotype in several diagnostic characteristics, including MBSR, DBR, and SRB, exhibiting only minor variation in small-scale morphological features. For instance, measurements such as PVSR, VSR, and NU all fall within the normal range of variation.

Etymology. The species is named after its type locality in Maerkang City, Sichuan Province, China. We suggested the common names "马尔康滑蜥" in Chinese and "Maerkang ground skink" in English for this species.

Distribution and habitat. Currently, this species is known only from Maerkang City. The holotype was collected in late May 2022. Its typical habitat consists of areas adjacent to small shrublands, where individuals use large rocks for shelter and bask on exposed rock surfaces when sunlight is available (Fig. 10). The species occurs sympatrically with *Gloydius angusticeps* and *Protobothrops jerdonii*.

Comparisons with congeners. In addition to its large genetic distances, *Scincella maerkangensis* sp. nov. can be distinguished from all known congeners based on distinct morphological characters. Notably, it differs from *Scincella jinchuanensis* sp. nov., *S. barbouri*, *S. doriae*, *S. modesta*, *S. formosensis*, *S. przewalskii*, and *S. wangyuezhaoi* by having fewer dorsal scale rows between dorsolateral stripes (DBR) 1/2+4+1/2 (vs. 1/2+6+1/2). It differs from *S. reevesii* by having fewer DBR 1/2+4+1/2 (vs. 1/2+8+1/2) (Table 5).

Figure 10. Type locality habitat of *Scincella maerkangensis* sp. nov. in Maerkang City, Sichuan Province, China.

Table 5. Measurements and scale counts of the type specimens of *Scincella maerkangensis* sp. nov. Abbreviations are detailed in the section of materials and methods.

Characters	Holotype	Paratypes		
	YBU250140	YBU250143	YBU250141	YBU250139
SVL	50.18	57.57	56.33	59.47
TAL	71.90	81.91	–	–
FLL	6.42	7.19	6.14	7.36
HLL	9.72	8.71	7.06	9.88
AGD	29.27	34.14	35.79	37.05
NU	3–3	4–3	3–3	3–3
SL	8–9	8–8	7–7	7–7
IfL	8–6	7–8	7–7	7–6
F4L	2.64	3.12	2.95	3.24
T4L	5.02	5.35	5.14	5.65
SC	7–5	5–4	4–5	6–4
SO	4–4	4–4	4–4	4–4
L	2–2	2–2	2–2	2–2
PN	0	0	0	0
MBSR	24	24	24	24
DBR	1/2+4+1/2	1/2+4+1/2	1/2+4+1/2	1/2+4+1/2
TEM	1+2/1+2	2+2/2+2	1+3/1+3	1+3/1+3
SRB	1	1	1	1
PVSR	60	60	58	67
T4S	14–15	15–15	15–15	14–14
F4S	11–11	10–10	11–12	10–11
GL	24	24	24	24
VSR	56	51	60	61
PF	2	2	2	2
FP	2	2	2	2
ADLS	straight	straight	straight	straight

The new species can also be distinguished from *Scincella jinchuanensis* sp. nov., *S. heishuiensis*, *S. chengduensis*, *S. qianica*, *S. alia*, and *S. doriae* by exhibiting 24 midbody scale-row (MBSR) (vs. 28 in *Scincella jinchuanensis* sp. nov., 28 in *S. heishuiensis*, 23 in *S. chengduensis*, 26 in *S. qianica*, 26–28 in *S. alia*, 30–32 in *S. doriae*). The new species can be further differentiated from *Scincella reevesii*, *Scincella modesta*, *Scincella doriae*, *S. schmidti*, *S. barbouri*, and *S. formosensis* by the appearance of dorso-lateral stripes, which are straight (vs. wavy). It differs from *S. doriae*, *Scincella jinchuanensis* sp. nov., and *S. schmidti* by having 14–15 T4S (vs. 11–12 in *S. schmidti*; 17–18 in *Scincella jinchuanensis* sp. nov.; 16–18 in *S. doriae*). It is distinct from *S. chengduensis* and *S. fansipanensis* by having more enlarged undivided lamellae beneath finger IV (10–12 vs. 8–9 in *S. chengduensis* and 7–9 in *S. fansipanensis*). The new species differs from *S. barbouri*, *S. huanrenensis*, and *S. tsinlingensis* in paravertebral scale-row count (58–67 vs. 70–79 in *S. barbouri*, 52–60 in *S. huanrenensis*, and 70–90 in *S. tsinlingensis*). The new species can be further differentiated from *S. chengduensis* by a ventral scale-row count of 51–61 (vs. 42–44) and can be distinguished from *S. chengduensis* by having more gulars 24 (vs. 21–22).

The new species is most similar to *Scincella wangyuezhaoi* but can be diagnosed from the latter by its unique ventrolateral coloration (uniformly distributed black-ish-gray hue with gradually sparse spotting on the lower body vs. densely covered black spots presenting a uniform grayish-brown appearance across the entire ventrolateral region). *Scincella maerkangensis* sp. nov. also differs in characteristics of MBSR, DBR, and scale rows covered by dorsolateral stripes (SRB), specifically: MBSR 24 (vs. 27–30), DBR 1/2+4+1/2 (vs. 1/2+6+1/2), and SRB 1 (vs. 3).

Discussion

The family Scincidae, one of the most diverse groups of lizards, currently comprises over 1,700 species distributed across both the Eastern and Western Hemispheres (Uetz et al. 2025). This high species diversity and wide geographical distribution represent considerable challenges for comprehensive sampling and robust phylogenetic reconstruction. As a result, the phylogeny and biogeography of this family remain incompletely resolved at multiple taxonomic levels. Recent advances have improved our understanding of the classification and phylogeny of the genus *Scincella*. Nevertheless, the taxonomy of *Scincella* species in China continues to be problematic, largely due to difficulties in specimen acquisition, which has resulted in scarce genetic and morphological data for certain taxa. In this study, through integrated genetic and morphological analyses, we describe two new species of this genus from western China, raising the total number of recognized species in the genus to 53, 19 of which are known from China.

Although molecular phylogenies based on three mitochondrial fragments have clarified some lower-level relationships within *Scincella*, higher-level classification remains unresolved, underscoring the limitations of the current taxonomic framework. Furthermore, the taxonomic status of several recognized species, including *S. tsinlingensis*, *S. huanrenensis*, *S. potanini*, and *S. monticola*, remains controversial and requires further systematic investigation.

Phylogenetic analysis reveals that the two new species form a distinct clade with *S. heishuiensis*, *S. wangyuezhaoi*, and other recently described species (PP = 0.98). The uncorrected genetic distance (*p*-distance) between the two new species, based on 16S rRNA, is 6.74%. Geographically, the type localities of these species are all situated in the northern HDM. They exhibit a parapatric or closely proximate distribution and occupy similar habitats, yet show significant genetic and morphological differentiation. The recent surge in descriptions of new *Scincella* species from the HDM region underscores the need to investigate the drivers of this diversification. Future studies should employ expanded specimen sampling, additional genetic markers, and genomic-scale data.

Acknowledgments

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